

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID: ssspta1649jxm

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TERMINAL (ENTER 1, 2, 3, OR ?):2

NEWS 46 Feb 26 NTIS now allows simultaneous left and right truncation
NEWS 47 Feb 26 PCTFULL now contains images
NEWS 48 Mar 04 SDI PACKAGE for monthly delivery of multifile SDI results
NEWS 49 Mar 19 APOLLIT offering free connect time in April 2003
NEWS 50 Mar 20 EVENTLINE will be removed from STN
NEWS 51 Mar 24 PATDPAFULL now available on STN
NEWS 52 Mar 24 Additional information for trade-named substances without
structures available in REGISTRY
NEWS 53 Mar 24 Indexing from 1957 to 1966 added to records in CA/CAPLUS

NEWS EXPRESS January 6 CURRENT WINDOWS VERSION IS V6.01a,
CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002

NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
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NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

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FILE 'HOME' ENTERED AT 13:46:06 ON 03 APR 2003

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=> s bandman olga /au
L1 344 BANDMAN OLGA

```
=> tang tom y /au
TANG IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (>).
```

=> s tang tom y /au
1.2 29 TANG TOM Y

=> s hillman jennifer l /au
L3 527 HILLMAN JENNIFER L

=> guegler karl j /au
GUEGLER IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s guegler karl j /au
L4 264 GUEGLER KARL J

=> s corley meil c /au
L5 0 CORLEY MEIL C

=> s gorgone gina a /au
L6 45 GORGONE GINA A

=> s azimzai yalda /au
L7 135 AZIMZAI YALDA

=> s lu dyung aina / au
MISSING OPERATOR
MISSING OPERATOR
MISSING OPERATOR
MISSING OPERATOR

=> s lu dyung aina /au
L8 0 LU DYUNG AINA

=> s antibody same protein same kinase
L9 0 ANTIBODY SAME PROTEIN SAME KINASE

=> s antibody (s) protein (s) kinase
L10 32422 ANTIBODY (S) PROTEIN (S) KINASE

09870962 Results

SEQ ID NO: 5

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	327	100.0	327	21	AAY76752		Human protein kina
2	327	100.0	327	22	AAE06210		Human protein kina
3	157	48.0	260	22	AAU17290		Novel signal trans
4	157	48.0	325	23	ABB06096		Human NS protein s
5	157	48.0	348	22	AAM93467		Human polypeptide,
6	157	48.0	367	20	AAY55962		Human STLK6 protei
7	157	48.0	373	20	AAY55961		Full length human
8	157	48.0	393	23	ABB06097		Human NS protein s
9	157	48.0	394	22	AAM93325		Human polypeptide,
10	150	45.9	262	22	AAU87400		Novel central nerv
11	150	45.9	274	20	AAY55930		Human STLK5 protei
12	150	45.9	283	22	AAU87285		Novel central nerv
13	150	45.9	290	22	AAU87580		Novel central nerv
14	150	45.9	290	22	AAU17292		Novel signal trans
15	121	37.0	138	22	ABG14218		Novel human diagno
16	116	35.5	177	21	AAB41582		Human ORFX ORF1346
17	93	28.4	336	22	ABG14224		Novel human diagno
18	91	27.8	238	22	AAU87292		Novel central nerv
19	91	27.8	238	22	AAU17259		Novel signal trans
20	71	21.7	128	22	ABG14219		Novel human diagno

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	327	100.0	327	3	US-09-173-581-5		Sequence 5, Appli
2	327	100.0	327	4	US-09-420-915-5		Sequence 5, Appli
3	7	2.1	146	4	US-09-509-902A-10		Sequence 10, Appli
4	7	2.1	346	4	US-08-887-534A-68		Sequence 68, Appli
5	7	2.1	481	4	US-09-537-168-2		Sequence 2, Appli
6	7	2.1	483	1	US-08-468-700-34		Sequence 34, Appli
7	7	2.1	483	1	US-08-645-971-2		Sequence 2, Appli
8	7	2.1	483	2	US-08-468-220-32		Sequence 32, Appli
9	7	2.1	483	2	US-08-468-220-36		Sequence 36, Appli
10	7	2.1	483	2	US-08-468-698-32		Sequence 32, Appli
11	7	2.1	483	2	US-08-468-698-36		Sequence 36, Appli
12	7	2.1	483	2	US-08-704-706A-34		Sequence 34, Appli
13	7	2.1	483	2	US-08-600-908A-13		Sequence 13, Appli
14	7	2.1	483	3	US-08-890-383-3		Sequence 3, Appli
15	7	2.1	483	3	US-08-683-838A-13		Sequence 13, Appli
16	7	2.1	483	3	US-08-914-679A-3		Sequence 3, Appli
17	7	2.1	483	4	US-09-182-859-2		Sequence 2, Appli
18	7	2.1	483	4	US-09-170-670-4		Sequence 4, Appli
19	7	2.1	483	4	US-09-193-068-4		Sequence 4, Appli
20	7	2.1	483	4	US-09-183-412-4		Sequence 4, Appli
21	7	2.1	483	4	US-08-985-659-35		Sequence 35, Appli
22	7	2.1	483	4	US-09-264-097-2		Sequence 2, Appli
23	7	2.1	483	4	US-08-194-664A-32		Sequence 32, Appli
24	7	2.1	483	4	US-08-194-664A-36		Sequence 36, Appli
25	7	2.1	483	4	US-09-291-023A-21		Sequence 21, Appli
26	7	2.1	483	4	US-09-290-734-4		Sequence 4, Appli
27	7	2.1	483	4	US-09-537-168-4		Sequence 4, Appli
28	7	2.1	483	4	US-09-672-459-2		Sequence 2, Appli
29	7	2.1	483	4	US-09-636-252A-13		Sequence 13, Appli
30	7	2.1	483	5	PCT-US94-01553A-32		Sequence 32, Appli
31	7	2.1	483	5	PCT-US94-01553A-36		Sequence 36, Appli
32	7	2.1	483	5	PCT-US95-10426-32		Sequence 32, Appli
33	7	2.1	483	5	PCT-US95-10426-36		Sequence 36, Appli
34	7	2.1	487	2	US-08-468-220-37		Sequence 37, Appli

35	7	2.1	487	2	US-08-468-698-37	Sequence 37, Appl
36	7	2.1	487	4	US-08-194-664A-37	Sequence 37, Appl
37	7	2.1	487	5	PCT-US94-01553A-37	Sequence 37, Appl
38	7	2.1	487	5	PCT-US95-10426-37	Sequence 37, Appl
39	7	2.1	511	1	US-08-468-700-35	Sequence 35, Appl
40	7	2.1	511	1	US-08-645-971-3	Sequence 3, Appli
41	7	2.1	511	2	US-08-468-220-33	Sequence 33, Appl
42	7	2.1	511	2	US-08-468-698-33	Sequence 33, Appl
43	7	2.1	511	2	US-08-704-706A-35	Sequence 35, Appl
44	7	2.1	511	3	US-08-890-383-2	Sequence 2, Appli
45	7	2.1	511	3	US-08-890-383-4	Sequence 4, Appli

RESULT 3
 US-09-509-902A-10
 ; Sequence 10, Application US/09509902A
 ; Patent No. 6387676
 ; GENERAL INFORMATION:
 ; APPLICANT: Virca, Duke
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Anderson, Dirk M.
 ; APPLICANT: Marken, John S.
 ; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase Functions
 ; FILE REFERENCE: 2877-US
 ; CURRENT APPLICATION NUMBER: US/09/509,902A
 ; CURRENT FILING DATE: 1999-08-03
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 146
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (140)..(140)
 ; OTHER INFORMATION: UNSURE
 US-09-509-902A-10

```
Query Match          2.1%;  Score 7;  DB 4;  Length 146;
Best Local Similarity 100.0%;  Pred. No. 29;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
Qy      66 LFNHPNI 72
      ||||| |
Db      9 LFNHPNI 15
```

RESULT 4
 US-08-887-534A-68
 ; Sequence 68, Application US/08887534A
 ; Patent No. 6455323
 ; GENERAL INFORMATION:
 ; APPLICANT: Holden, David W.
 ; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive/6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,534A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/33996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-887-534A-68

Query Match 2.1%; Score 7; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 LAIAYIL 118
|||||||
Db 19 LAIAYIL 25

RESULT 5

US-09-537-168-2

; Sequence 2, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-537-168-2

Query Match 2.1%; Score 7; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 SVANSGL 265
|||||||
Db 416 SVANSGL 422

RESULT 6

US-08-468-700-34

; Sequence 34, Application US/08468700
; Patent No. 5736499
; GENERAL INFORMATION:
; APPLICANT: COLIN MITCHINSON
; APPLICANT: CAROL A. REQUADT
; APPLICANT: TRACI H. ROOP

; APPLICANT: LEIF P. SOLHEIM
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,700
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 252
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7555
; TELEFAX: (415) 742-7217
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-468-700-34

Query Match 2.1%; Score 7; DB 1; Length 483;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 259 SVANSGL 265
|||
Db 418 SVANSGL 424

RESULT 7
US-08-645-971-2
; Sequence 2, Application US/08645971
; Patent No. 5763385
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Alpha-Amylases Having Altered
; TITLE OF INVENTION: Calcium Binding Properties
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,971
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus licheniformis
US-08-645-971-2

Query Match 2.1%; Score 7; DB 1; Length 483;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 SVANSGL 265
|||||||
Db 418 SVANSGL 424

RESULT 8

US-08-468-220-32

; Sequence 32, Application US/08468220
; Patent No. 5824532
; GENERAL INFORMATION:
; APPLICANT: Antrim, Richard L.
; APPLICANT: Barnett, Christopher
; APPLICANT: Mitchinson, Colin
; APPLICANT: Power, Scott D.
; APPLICANT: Requadt, Carol
; APPLICANT: Solheim, Leif P.
; TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,220
; FILING DATE: 06-JUN-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/194,664
; FILING DATE: 10-FEB-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/016,395
; FILING DATE: 11-FEB-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher L.
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC220D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7555
; TELEFAX: (415) 742-7217
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-468-220-32

Query Match 2.1%; Score 7; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 SVANSGL 265
|||||||
Db 418 SVANSGL 424

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	8	2.4	119	2	E84559	probable peptidyl-
2	8	2.4	432	2	B96515	hypothetical prote
3	8	2.4	434	2	C96515	hypothetical prote
4	8	2.4	842	2	B55853	outer membrane ush
5	7	2.1	84	2	C69499	virulence associat
6	7	2.1	101	2	F69223	hypothetical prote
7	7	2.1	127	2	G81688	hypothetical prote
8	7	2.1	135	1	B49205	virulence-associat
9	7	2.1	137	2	S46307	cytochrome b5 - ri
10	7	2.1	178	2	S03629	neurogenic gene co
11	7	2.1	189	2	C64595	hypothetical prote
12	7	2.1	205	2	D71918	hypothetical prote
13	7	2.1	210	2	B87429	nitroreductase fam
14	7	2.1	212	2	S27856	cAMP-inducible pro
15	7	2.1	229	2	S72165	hypothetical prote
16	7	2.1	230	2	C71548	probable ABC trans
17	7	2.1	231	2	AE2164	hypothetical prote
18	7	2.1	245	2	G90282	hypothetical prote
19	7	2.1	294	2	T08408	transcription fact
20	7	2.1	320	2	H89970	hypothetical prote
21	7	2.1	323	2	H90282	hypothetical prote
22	7	2.1	325	2	C72289	oligopeptide ABC t
23	7	2.1	336	2	A24430	glyceraldehyde-3

RESULT 9

Q39908

ID Q39908 PRELIMINARY; PRT; 332 AA.
 AC Q39908;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE cAMP-dependent protein kinase.
 OS Gonyaulax polyedra.
 OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Gonyaulacaceae;
 OC Gonyaulax.
 OX NCBI_TaxID=2913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=70;
 RA Salois P., Morse D.;
 RT "Isolation and characterization of a cAMP-dependent protein kinase
 RT cDNA from the marine dinoflagellate Gonyaulax polyedra.";
 RL Plant Mol. Biol. 0:0-0 (1995).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; L41064; AAA64341.1; -.
 DR HSSP; P05132; ICTP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 332 AA; 37340 MW; B5CA4D5223D4E1A3 CRC64;

Query Match 2.4%; Score 8; DB 10; Length 332;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 302 LQRNP DAR 309
| | | | | | |
Db 242 LQRNP DAR 249

09870962Results
SEQ ID NO: 5

Result No.	Score	Query Match	Length	DB	ID	Description
1	1744	100.0	327	21	AAY76752	Human protein kina
2	1744	100.0	327	22	AAE06210	Human protein kina
3	1730	99.2	348	22	AAM93467	Human polypeptide,
4	1621	92.9	373	20	AAY55961	Full length human
5	1621	92.9	394	22	AAM93325	Human polypeptide,
6	1555	89.2	367	20	AAY55962	Human STLK6 protei
7	1543	88.5	325	23	ABB06096	Human NS protein s
8	1425.5	81.7	393	23	ABB06097	Human NS protein s
9	1187	68.1	260	22	AAU17290	Novel signal trans
10	1176	67.4	290	22	AAU87580	Novel central nerv
11	1176	67.4	290	22	AAU17292	Novel signal trans
12	1171	67.1	336	22	ABG14224	Novel human diagno
13	1148	65.8	283	22	AAU87285	Novel central nerv
14	1101	63.1	274	20	AAY55930	Human STLK5 protei
15	905	51.9	177	21	AAB41582	Human ORFX ORF1346
16	873	50.1	262	22	AAU87400	Novel central nerv
17	817	46.8	238	22	AAU87292	Novel central nerv
18	817	46.8	238	22	AAU17259	Novel signal trans
19	756.5	43.4	418	22	AAB95756	Human protein sequ
20	756.5	43.4	418	22	AAG67609	Amino acid sequenc
21	756.5	43.4	421	22	AAM40545	Human polypeptide
22	744.5	42.7	418	21	AAY44238	Human cell signall
23	720.5	41.3	401	22	AAB85517	Human protein kina
24	654	37.5	234	21	AAB51909	Human secreted pro
25	639	36.6	138	22	ABG14218	Novel human diagno
26	610.5	35.0	128	22	ABG14219	Novel human diagno
27	571.5	32.8	280	22	AAM38759	Human polypeptide

RESULT 1
AAY76752
ID AAY76752 standard; Protein; 327 AA.
XX
AC AAY76752;
XX
DT 17-APR-2000 (first entry)
XX
DE Human protein kinase homologue, PKH-5.
XX
KW Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS;
KW autoimmune disorder; inflammatory disorder; reproductive defect; asthma;
KW diabetes mellitus; infertility; ovulatory defect; endometriosis;
KW polycystic ovary syndrome.
XX
OS Homo sapiens.
XX
PN US6013455-A.
XX
PD 11-JAN-2000.
XX
PF 15-OCT-1998; 98US-0173581.
XX
PR 15-OCT-1998; 98US-0173581.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Yue H, Yang YT, Corley NC, Gorgone GA, Azimzai Y;
PI Lu DAM, Bandman O, Guegler KJ;
XX
DR WPI; 2000-136321/12.
DR N-PSDB; AAZ86796.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory

PT disorders and reproductive defects -

XX

PS Claim 1; Column 49-52; 38pp; English.

XX

CC This sequence represents a human protein kinase homolog (PKH) of the
CC invention. The PKH sequences may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate PKH expression such
CC as cancers, autoimmune/inflammatory disorders and reproductive defects.
CC They may be used to treat disorders associated with decreased PKH
CC expression such as cancers (e.g. lymphoma, melanoma and cancers of the
CC breast lung and prostate), autoimmune/inflammatory disorders
CC (e.g. AIDS, asthma and diabetes mellitus), and reproductive
CC defects (e.g. infertility, ovulatory defects, endometriosis and
CC polycystic ovary syndrome). The DNA may be administered to treat diseases
CC by rectifying mutations or deletions in a patient's genome that affect
CC the activity of PKH by expressing inactive proteins or to supplement the
CC patients own production of PKH polypeptides. Additionally, the DNA may be
CC used to produce PKH, according to standard recombinant DNA methodology,
CC by inserting the nucleic acids into a host cell and culturing the cell to
CC express the protein. Conversely, antisense nucleic acid molecules may be
CC administered to down regulate PKH expression by binding with the cells
CC own PKH genes and preventing their expression. The DNA, and antisense
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acid sequences in samples,
CC and hence which patients may be in need of restorative therapy. They may
CC also be used to study the expression and function of PKH polypeptides and
CC their role in metabolism. The PKH polypeptides may be used as antigens in
CC the production of antibodies against PKH and in assays to identify
CC modulators (agonists and antagonists) of PKH expression and activity. The
CC anti-PKH antibodies and PKH antagonists may also be used to down regulate
CC PKH expression and activity. The anti-PKH antibodies may also be used as
CC diagnostic agents for detecting the presence of PKH polypeptides in
CC samples.

XX

SQ Sequence 327 AA;

Query Match 100.0%; Score 1744; DB 21; Length 327;
Best Local Similarity 100.0%; Pred. No. 2e-174;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRINLEACSNEMVTFLQGE 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRINLEACSNEMVTFLQGE 60

Qy 61 LHVSKLFNHPNIVPYRATFIADNELWVVTSMAYGSAKDLICHTFMDGMNELAIAYILQG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LHVSKLFNHPNIVPYRATFIADNELWVVTSMAYGSAKDLICHTFMDGMNELAIAYILQG 120

Qy 121 VLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRTTSLMISHGQRQRVVHDFPKYSV 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 VLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRTTSLMISHGQRQRVVHDFPKYSV 180

Qy 181 KVLPWLSPEVLQQNLQGYDAKSDIYSGVITACELANGHVPFKDMPATQMLLEKLNGTVPC 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 KVLPWLSPEVLQQNLQGYDAKSDIYSGVITACELANGHVPFKDMPATQMLLEKLNGTVPC 240

Qy 241 LLDTSTI PAEEELTMSPSRSVANSGLSDSLLTSTPRPSNGDSPSHPYHRTFSPHFHHFVEQ 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 LLDTSTI PAEEELTMSPSRSVANSGLSDSLLTSTPRPSNGDSPSHPYHRTFSPHFHHFVEQ 300

Qy 301 CLQRNP DARYPCWPGPGLRESRGCSGG 327

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 CLQRNP DARYPCWPGPGLRESRGCSGG 327

RESULT 14

AY55930

ID AY55930 standard; Protein; 274 AA.

XX

AC AY55930;

XX
DT 18-FEB-2000 (first entry)
XX
DE Human STLK5 protein.
XX
KW Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;
KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;
KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;
KW antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW myocardial infarction; cardiovascular disease; stroke; renal failure;
KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW mesangial disorder; growth regulation; wound healing; T cell activation;
KW immunosuppressant.
XX
OS Homo sapiens.
XX
PN WO9953036-A2.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US08150.
XX
PR 14-APR-1998; 98US-0081784.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman G, Martinez R, Whyte D;
XX
DR WPI; 1999-611301/52.
DR N-PSDB; AAZ40482.
XX
PT Novel kinase-related polypeptides used for the diagnosis and treatment
PT of kinase-related diseases and disorders -
XX
PS Claim 12; Page 263-264; 387pp; English.
XX
CC This sequence represents a novel STE20-related protein kinase. The
CC invention relates to nucleic acid molecule encoding a kinase polypeptide
CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
CC ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC identify agonists and antagonists, and to raise antibodies. The
CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
CC polypeptides, antibodies, antagonists and agonists may be used to treat
CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.
CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC infarction, cardiovascular disease, stroke, renal failure, oxidative
CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC mellitus, fibrotic and mesangial disorders. The proteins may also be
CC useful for cell growth regulation (e.g. in wound healing), T cell
CC activation, mitosis control, and as immunosuppressants.
XX
SQ Sequence 274 AA;

Query Match 63.1%; Score 1101; DB 20; Length 274;
Best Local Similarity 99.0%; Pred. No. 6.2e-107;
Matches 208; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 100 LICTHFMDGMNELAIAYILQGVVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRTT 159

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 LICTHFMDGMNELAIAYILQGVVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSN 60

Qy 160 LSMISHGQRQRVVHDFPKYSVKLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHV 219
 |||||||
 Db 61 LSMISHGQRQRVVHDFPKYSVKLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHV 120
 |||||||
 Qy 220 PFKDMPATQMLLEKLNGTVPCLLDSTIPAEELTMSPSRSVANSGLSDSLLTSTPRPSNG 279
 |||||||
 Db 121 PFKDMPATQMLLEKLNGTVPCLLDSTIPAEELTMSPSRSVANSGLSDSLLTSTPRPSNG 180
 |||||||
 Qy 280 DSPSHPYHRTFSPHFHHFVEQCLQRNPNDAR 309
 |||||||
 Db 181 DSPSHPYHRTFSPHFHHFVEQCLQRNPNDAR 210

Issued:

SUMMARIES

%

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1744	100.0	327	3	US-09-173-581-5	Sequence 5, Appli
2	1744	100.0	327	4	US-09-420-915-5	Sequence 5, Appli
3	306	17.5	270	2	US-08-852-743-5	Sequence 5, Appli
4	306	17.5	270	3	US-09-185-370-5	Sequence 5, Appli
5	301	17.3	487	2	US-08-712-709-8	Sequence 8, Appli
6	301	17.3	487	3	US-09-111-444-8	Sequence 8, Appli
7	301	17.3	487	4	US-09-541-228-8	Sequence 8, Appli
8	287.5	16.5	403	2	US-08-712-709-3	Sequence 3, Appli
9	287.5	16.5	403	3	US-09-111-444-3	Sequence 3, Appli
10	287.5	16.5	403	4	US-09-541-228-3	Sequence 3, Appli
11	278	15.9	416	2	US-09-211-930-11	Sequence 11, Appl
12	278	15.9	416	3	US-09-340-993-11	Sequence 11, Appl
13	278	15.9	416	4	US-09-468-442-11	Sequence 11, Appl
14	278	15.9	431	2	US-09-211-930-5	Sequence 5, Appli
15	278	15.9	431	3	US-09-340-993-5	Sequence 5, Appli
16	278	15.9	431	4	US-09-152-406-3	Sequence 3, Appli
17	278	15.9	431	4	US-09-468-442-5	Sequence 5, Appli
18	277	15.9	416	2	US-09-211-930-3	Sequence 3, Appli
19	277	15.9	416	3	US-09-340-993-3	Sequence 3, Appli
20	277	15.9	416	4	US-09-468-442-3	Sequence 3, Appli